WEST Search History

DATE: Saturday, August 24, 2002

Set Name side by side	Query	Hit Count	Set Name result set
	DB=USPT; PLUR=YES; OP=OR		
L23	(204/450)!.ccls	386	L23
L22	(435/6)!.ccls	13933	L22
L21	(800/295)!.ccls	436	L21
L20	(800/286)!.ccls	184	L20
L19	(800/285)!.ccls	63	L19
L18	(800/278)!.ccls	851	L18
L17	(435/419)!.ccls	1475	L17
L16	(536/24.5)!.ccls	1634	L16
L15	(536/23.1)!.ccls	8935	L15
L14	gene same silencing same plant same RNA same 25	2	L14
L13	gene same silencing same plant same RNA	25	L13
L12	gene same silencing same plant	337	L12
L11	l7 and l9	0	L11
L10	l6 and l9	0	L10
L9	short adj RNA adj molecules	17	L9
L8	short adj RNA molecules	313331	L8
L7	(post-transcriptional adj gene adj silencing or PTGS)	417	L7
L6	gene adj silencing	134	L6
L5	gene silencing	70775	L5
L4	L3 and RNA	54	L4
L3	l1 and L2	62	L3
L2	polyacrylamide same 15% same 7M adj urea	67	L2
L1	electrophoresis	38316	L1

END OF SEARCH HISTORY

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FILE 'HOME' ENTERED AT 11:08:11 ON 24 AUG 2002

=> file medline, biosis, embase, scisearch, caplus

COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
FULL ESTIMATED COST                                         0.21       0.21

FILE 'MEDLINE' ENTERED AT 11:08:33 ON 24 AUG 2002

FILE 'BIOSIS' ENTERED AT 11:08:33 ON 24 AUG 2002
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FILE 'SCISEARCH' ENTERED AT 11:08:33 ON 24 AUG 2002
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FILE 'CAPLUS' ENTERED AT 11:08:33 ON 24 AUG 2002
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
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=> s gene silencing

L1         6696 GENE SILENCING

=> s post transcriptional gene silencing

L2          621 POST TRANSCRIPTIONAL GENE SILENCING

=> s l1 or l2

L3         6696 L1 OR L2

=> s RNA

L4      1449880 RNA

=> s l4 and (short RNA molecules or SRM)

L5           51 L4 AND (SHORT RNA MOLECULES OR SRM)

=> s l5 and (21 nucleotides or 25 nucleotides)

L6            0 L5 AND (21 NUCLEOTIDES OR 25 NUCLEOTIDES)

=> s l5 and (21nt or 25nt)

L7            0 L5 AND (21NT OR 25NT)

=> s l5 and (21 bases or 25 bases)

L8            0 L5 AND (21 BASES OR 25 BASES)

=> l3 and l5

L3 IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
```

for a list of commands available to you in the current file, enter "HELP COMMANDS" at an arrow prompt (=>).

=> s l3 and l5

L9 3 L3 AND L5

=> dup rem

ENTER L# LIST OR (END):l5

PROCESSING COMPLETED FOR L5
L10 24 DUP REM L5 (27 DUPLICATES REMOVED)

=> s l5 and polyacrylamide

L11 0 L5 AND POLYACRYLAMIDE

=> s l4 and polyacrylamide

L12 33288 L4 AND POLYACRYLAMIDE

=> s l4 and 15% polyacrylamide

L13 57 L4 AND 15% POLYACRYLAMIDE

=> s l13 and 7% urea

L14 0 L13 AND 7% UREA

=> s l13 and 7M urea

L15 1 L13 AND 7M UREA

=> d l9 tot ibib abs

```
=> dup rem

ENTER L# LIST OR (END):l13

PROCESSING COMPLETED FOR L13
L16           29 DUP REM L13 (28 DUPLICATES REMOVED)
```

L16 ANSWER 3 OF 29 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 2

ACCESSION NUMBER: 1996:283623 BIOSIS
DOCUMENT NUMBER: PREV199699005979
TITLE: Analysis of a tRNA gene-like sequence (t-element) with TTA at the anticodon position in the mitochondrial DNA of Dictyostelium discoideum.
AUTHOR(S): Pi, Min; Angata, Kiyohiko; Ikemura, Toshimichi; Yanagisawa, Kaichiro; Tanaka, Yoshimasa (1)
CORPORATE SOURCE: (1) Inst. Biol. Sci., Univ. Tsukuba, Tsukuba, Ibaraki 305 Japan
SOURCE: Journal of Plant Research, (1996) Vol. 109, No. 1093, pp. 1-6.
ISSN: 0918-9440.
DOCUMENT TYPE: Article
LANGUAGE: English

AB During the course of mitochondrial DNA sequencing of Dictyostelium discoideum, a sequence with a tRNA-like structure and two genes for tRNA-Gln(UUG) and tRNA-Trp(CCA) were found downstream of the gene for large subunit rRNA. The existence of tRNA-Trp with CCA anticodon supports the finding that UGA codon is not a tryptophan codon in D. discoideum mitochondria. Interestingly, the tRNA gene-like sequence (t-element) has TTA at the anticodon position. Northern blot analysis showed that, in low molecular mass mitochondrial **RNA** fraction of growth-phase cells and developmental stage cells, a mature transcript of the element could not be detected in the tRNA region on an urea-denatured 15% **polyacrylamide** gel, although there were several bands in the higher molecular mass region, indicating the actual transcription of the t-element. Southern blot analysis for total and mitochondrial DNA showed that the element exists as a single copy, only in the mitochondrial DNA but not in the nuclear DNA.

L16 ANSWER 5 OF 29 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1993:33656 CAPLUS
DOCUMENT NUMBER: 118:33656
TITLE: Direct quantification of picomolar concentrations of mRNAs by mathematical analysis of a reverse transcription/exponential polymerase chain reaction assay
AUTHOR(S): Wiesner, Rudolf J.
CORPORATE SOURCE: Dep. Physiol. II, Univ. Heidelberg, Heidelberg, W-6900, Germany
SOURCE: Nucleic Acids Res. (1992), 20(21), 5863-4
CODEN: NARHAD; ISSN: 0305-1048
DOCUMENT TYPE: Journal
LANGUAGE: English

AB It was recently shown that the no. of target mols. of PCR could be accurately detd. by measuring the molar concn. of a product, which accumulates in consecutive cycles by linear regression anal. Here, the method is extended to the measurement of the actual copy no. of mRNAs by performing quant. reverse transcription (RT) prior to amplification. The method was applied to the quantification of picomolar concns. of **RNA** extd. from frozen ventricles of female Sprague-Dawley rats (180 g) after reverse transcription and PCR using two 20 mer primers specific for and complementary to 2 isoforms of myosin heavy chain. Aliquots of 1 .mu.L were taken from the reaction after consecutive cycles and run on **15% polyacrylamide** gels, which were stained with ethidium bromide. The two product bands (77 bp for .alpha. and 99 bp for .beta. MHC) were isolated from the gel, slices were trimmed, dried at 80.degree. overnight in liq. scintillation vials and the incorporated radioactivity was detd. by liq. scintillation counting. The concn. of product accumulating in consecutive cycles, Nn (moles/.mu.L) can be calcd. from the incorporated radioactivity (cpm/mol), the specific radioactivity of the precursor dCTP (cpm/mol) in the reaction mixt. and the no. of dCTPs which can be incorporated into the newly synthesized stretch of the product, y, according to the equation: Nn(moles/.mu.L)=(cpm/.mu.L)/(cpm/mo l .times. y). The initial concn. of a double stranded DNA template at cycle zero, N0 (moles/.mu.L) and the efficiency of amplification, eff, can then be calcd. by linear regression anal. of the transformed equation describing product accumulation in the PCR: logNn = log eff .times. n + log N0. Since the rat ventricle contains .apprx.3.4 mg. of total **RNA**/g wet wt., and .apprx.8 .times. 107 myocytes/g wet wt., it can be calcd. that individual rat myocytes contain .apprx.26,000 and 6000 mols. of .alpha. and .beta. MHC mRNA, resp.

L16 ANSWER 8 OF 29 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 88021791 MEDLINE
DOCUMENT NUMBER: 88021791 PubMed ID: 2444136
TITLE: A simple and rapid solid-phase **RNA** sequencing method.
AUTHOR: Zhang Y; Liu W Y; Feng Y X; Wang T P
CORPORATE SOURCE: Department of Bioscience and Technology, Shanghai Jiao-Tong University, China.
SOURCE: ANALYTICAL BIOCHEMISTRY, (1987 Jun) 163 (2) 513-6. Journal code: 0370535. ISSN: 0003-2697.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198710
ENTRY DATE: Entered STN: 19900305
Last Updated on STN: 19900305
Entered Medline: 19871027

QP501.A6

AB A simple and rapid solid-phase **RNA** sequencing method has been developed based on Peattie's direct chemical method. 3'-Terminally labeled **RNA** was immobilized on DEAE-cellulose sheets and followed by specific modification with dimethyl sulfate, diethylpyrocarbonate, hydroxylamine (at pH 10 for the uridine and pH 5.5 for the cytidine reaction), and cleavage reaction with aniline. **RNA** fragments were washed from the DEAE-cellulose sheets using salt solutions, precipitated with ethanol, and separated by **15% polyacrylamide** gel electrophoresis. Due to the complete removal of the impurities normally present in the solution method, the higher resolution of the sequencing bands and lower background on the autoradiograph make this solid-phase technique more efficient. This solid-phase technique is much faster and more convenient than the original method.

L16 ANSWER 11 OF 29 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC. DUPLICATE 8

ACCESSION NUMBER: 1985:254662 BIOSIS
DOCUMENT NUMBER: BA79:34658
TITLE: PURIFICATION OF CUCUMBER PALE FRUIT VIROID.
AUTHOR(S): UYEDA I; SHIKATA E; SANO T
CORPORATE SOURCE: FACULTY OF AGRICULTURE, HOKKAIDO UNIVERSITY, SAPPORO 060, JAPAN.
SOURCE: ANN PHYTOPATHOL SOC JPN, (1984) 50 (3), 331-338.
CODEN: NSBGAM. ISSN: 0031-9473.
FILE SEGMENT: BA; OLD
LANGUAGE: English

S8599.A5

AB Cucumber pale fruit viroid was purified from infected cucumber leaves and stems. Nucleic acids were extracted from the frozen tissue by phenol-CHCl3-SDS [sodium dodecyl sulfate], and precipitated with ethanol. Polysaccharides were removed by ethylene glycol monomethyl ether treatment and phenolic substances by cetyltrimethyl ammonium bromide. After the 2 M LiCl soluble fraction was treated with DNase, low MW **RNA** were obtained. The viroid was further purified by CF-11 cellulose chromatography and **15% polyacrylamide** gel electrophoresis. Yield of the purified viroid was about 3-6 .mu.g/200 g of tissue. Five percent polyacrylamide gel electrophoresis of the purified viroid in the presence of urea revealed 2 bands associated with infectivity.

L16 ANSWER 12 OF 29 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1983:289222 BIOSIS
DOCUMENT NUMBER: BA76:46714
TITLE: ANOMALOUS CONDUCTIVITY ZONES IN ELECTROPHORESIS 3. EXPERIMENTAL TESTS OF THE THEORY.
AUTHOR(S): SPENCER M; KIRK J M
CORPORATE SOURCE: KING'S COLL. DEP. BIOPHYSICS, 26-29 DRURY LANE, LONDON WC2B 5RL, ENGLAND.
SOURCE: ELECTROPHORESIS, (1983) 4 (1), 46-52.
CODEN: ELCTDN. ISSN: 0173-0835.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB An assumption used in developing the basic theory, that ionic retardation factors are substantially independent of solute concentration, is tested and found valid. The results of electrophoresis [of tRNA] through **15% polyacrylamide** gels are in agreement with the theory. Zones of altered concentration appear in the presence of spermine tetrahydrochloride, sodium phosphate buffer (pH 7.2) or Tris-HCl (pH 7.0).

The use of ionic retardation factors and transport numbers deduced from conductivity measurements leads to correct prediction of the sign of concentration change in each case. The direction and velocity of migration of a low-concentration boundary can also be predicted, together with associated changes in pH. Further confirmation comes from a detailed analysis of published work on electrophoresis through sucrose gradients. The theoretical treatment is suitable for application to other systems (such as isoelectric focusing and isotachophoresis) where a gel is used as a stabilizing medium, and where effects of the kind discussed may produce

L16 ANSWER 17 OF 29 MEDLINE DUPLICATE 12
ACCESSION NUMBER: 79144731 MEDLINE
DOCUMENT NUMBER: 79144731 PubMed ID: 426779
TITLE: The postnatal methylation of transfer ribonucleic acid in brain. Evidence for the methylation of precursor transfer ribonucleic acid.
AUTHOR: Elahi E; Sellinger O Z
SOURCE: BIOCHEMICAL JOURNAL, (1979 Jan 1) 177 (1) 381-4.
Journal code: 2984726R. ISSN: 0264-6021.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 197905
ENTRY DATE: Entered STN: 19900315
Last Updated on STN: 19900315
Entered Medline: 19790516

cv/350/. 847

AB Incubation of 3-day-old rat brain with L-[methyl-3H]methionine resulted in the rapid labeling of low-molecular-weight cytoplasmic **RNA**. Electrophoresis in **15% polyacrylamide** gels provided evidence for the methylation of precursor tRNA molecules, and high-performance liquid chromatography demonstrated N2-methylguanine to be the predominant methylated base formed during the first 2 min of labelling.

L16 ANSWER 23 OF 29 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1977:134769 BIOSIS
DOCUMENT NUMBER: BA63:29633
TITLE: UTERO GLOBIN MESSENGER **RNA** TRANSLATION IN-VITRO.
AUTHOR(S): BULLOCK D W; WOO S L C; O'MALLEY B W
SOURCE: BIOL REPROD, (1976) 15 (4), 435-443.
CODEN: BIREBV. ISSN: 0006-3363.
FILE SEGMENT: BA; OLD
LANGUAGE: Unavailable

AB The mRNA coding for the progesterone-induced protein uteroglobin was extracted from endometrial tissue of rabbits in early pregnancy and enriched by binding to oligo-dT-cellulose. After translation in a cell-free system derived from wheat germ, total mRNA activity was assessed by measuring the incorporation of 35S-methionine into TCA-precipitable peptides and specific mRNA activity by immunoprecipitation with specific uteroglobin antibodies purified by affinity chromatography. Approximately 85% of total mRNA activity was recovered after dT-cellulose chromatography, 10% in the bound fraction and 75% in the unbound **RNA**, suggesting that the majority of endometrial mRNA species lacked poly A sequences of longer than about 20 residues. No poly A could be detected by 3H-poly U hybridization in the unbound fraction. In contrast, 69% of total mRNA activity was present in dT-bound **RNA** from rabbit liver. The immunoprecipitable cell-free translation products of endometrial dT-**RNA** gave a single peak of radioactivity on electrophoresis in **15% polyacrylamide** gels containing sodium dodecyl sulfate. The peak was completely displaced by the addition of an excess of authentic nonradioactive uteroglobin to the immunoprecipitation reaction and was absent from products of translation without added endometrial **RNA**. The cell-free product migrated more slowly than authentic uteroglobin, suggesting the synthesis of a precursor protein. So uteroglobin mRNA could be detected in dT-bound **RNA** from rabbit liver. The proportion of uteroglobin mRNA in endometrial dT-bound **RNA** reached a peak on day 4 of pregnancy and declined subsequently to nonpregnant levels on day 8, a pattern similar to that of ute

4 ANSWER 2 OF 2 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2000011521 MEDLINE
DOCUMENT NUMBER: 20011521
TITLE: A species of small antisense **RNA** in posttranscriptional **gene silencing** in plants [see comments].
COMMENT: Comment in: Science 1999 Oct 29;286(5441):886
AUTHOR: Hamilton A J; Baulcombe D C
CORPORATE SOURCE: Sainsbury Laboratory, John Innes Centre, Colney Lane, Norwich NR4 7UH, UK.
SOURCE: SCIENCE, (1999 Oct 29) 286 (5441) 950-2.
Journal code: UJ7. ISSN: 0036-8075.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Cancer Journals
ENTRY MONTH: 200001
ENTRY WEEK: 20000104
AB Posttranscriptional **gene silencing** (PTGS) is a nucleotide sequence-specific defense mechanism that can target both cellular and viral mRNAs. Here, three types of transgene-induced PTGS and one example of virus-induced PTGS were analyzed in plants. In each case, antisense **RNA** complementary to the targeted mRNA was detected. These **RNA** molecules were of a uniform length, estimated at **25 nucleotides**, and their accumulation required either transgene sense transcription or **RNA** virus replication. Thus, the 25-nucleotide antisense **RNA** is likely synthesized from an **RNA** template and may represent the specificity determinant of PTGS.

WEST Search History

DATE: Sunday, August 25, 2002

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT; PLUR=YES; OP=OR			
L2	(435/468).!ccls	955	L2
L1	(435/320.1).!ccls	13109	L1

END OF SEARCH HISTORY